nucleotide sequence specific of an organism with a signal resulting from a hybridization by complementary base pairing between the target nucleotide sequence and its corresponding capture nucleotide sequence is disclosed. The capture nucleotide sequence is bound to the insoluble solid support at a specific location on an array having a density of at least 4 different bound single stranded capture nucleotide sequences/cm^2. The location of the signal on the array allows identification or quantification of the organism.

COMMENTS

The specific changes to the abstract are shown on a separate sheet of paper attached hereto entitled **VERSION WITH MARKINGS TO SHOW CHANGES MADE**, which follows the signature page of this amendment. On this paper, the insertions are underlined, while the ~~deletions are struck through~~.

Please charge any additional fees, including any fees for additional extension of time, or credit overpayment to Deposit Account No. 11-1410.

Respectfully submitted,

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VERSION WITH MARKINGS TO SHOW CHANGES MADE

~~The present invention is related to an identification and/or quantification method of a biological (micro)organism or part of it (possibly present in a biological sample) by a detection of~~A method for identifying or quantifying an organism by a detecting its nucleotide sequence among at least 4 other homologous sequences~~and comprising the steps of:~~

~~- possibly extracting original nucleotide sequences (1) from the (micro)organism;~~

~~- amplifying or copying with a unique pair of primer(s), at least part of original nucleotide sequences (1) into target nucleotide sequences (2) to be detected;~~

~~- possibly labelling said target nucleotide sequences (2);~~

~~- putting into contact the labelled target nucleotide sequences (2)~~comprising amplifying nucleic acids from the organism to generate target nucleotide sequences to be detected; contacting the target nucleotide sequences with single stranded capture nucleotide sequences~~(3)~~ bound by a single predetermined link to an insoluble solid support~~(4), preferably a non porous solid support,~~

-and discriminating the binding of a target nucleotide sequence~~(2)~~ specific of an organism ~~or part of it by detecting, quantifying and/or recording~~with a signal resulting from a hybridization by complementary base pairing between the target nucleotide sequence~~(2)~~ and its corresponding capture nucleotide sequence~~(3),~~

~~- wherein said~~is disclosed. The capture nucleotide sequence ~~(3) being~~is bound to the insoluble solid support~~(4)~~ at a specific location ~~according to~~on an~~array, said~~ array having a density of at least 4 different bound single stranded capture nucleotide ~~sequences/cm^2 of solid support surface and~~sequences/cm^2. The location of the signal on the array allows identification or quantification of the organism.

~~wherein the binding between the target nucleotide sequence and its corresponding capture nucleotide sequence forms (will result in) said signal at the expected location, the detection of a single signal allowing a discrimination of the target nucleotide sequence specific of an organism or part of it from homologous nucleotide sequences.~~